

16/19

MOUSE

1L - 13 $\alpha$  HUMAN

HUMAN

1L - 13 $\alpha$  MOUSE

1 MEWPRLCGLWALLLCAGGGGGGGAAAPTETQPPVTNLSVSVENLCTVIW 50 ←  
| . | | . | : | | | . . . . | : | | | | | | | | | | | | | | | |  
1 MARPALLGELLVLLL..WTATVGQVAAATEVQPPVTNLSVSVENLCTIIW 48 ←  
  
51 TWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGS 100  
| | . | | | | | . | : | | | | | | | | | | | | | | | | | | | | | |  
49 TWSPEGASPNCTLRYFSHFDDQDKKIAPETHRKEELPLDEKICLQVGS 98  
  
101 QCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGR 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
99 QCSANESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKCSWLPGR 148  
  
151 NTSPDTNYTLYYWHRSLEKIHQENIFREGQYFGCSFDLTKVKDSSFEQH 200  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
149 NTSPDTHYTLYYWYSSLEKSROENIYREGQHIACSFKLTKV.EPSFEHQ 197  
  
201 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLYVQWENP 250  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
198 NVQIMVKDNAGKIRPSCKIVSLTSYVKPDPPHIKHLLLNGALLVQWKNP 247  
  
251 QNFISRCLFYEVNVNSQTEHNVFYVQEAKCENPEFERNVENTSCFMVP 300  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
248 QNFRSRCLTYEVNVNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLP 297  
  
301 GVLPTDLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLL 350  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
298 GVLADAVYTVRVRVKTNKLCFDDNKLWSDWSEAQSIGKEQNSTFYTTMLL 347  
  
351 IVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDTLHWK 400  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
348 TIPVFVAVAVIILLFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDTLHWK 397  
  
401 KYDIYEKQTKEETDSVVLIELKKASQ 427  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
398 KYDIYEKQSKEETDSVVLIELKKAAP 424

FIG. 7b

IL-13R $\alpha$  SOURISIL-13R $\alpha$  HUMAIN

1 MEWPRLCGLWALLLCAGGGGGGGAAPTETQPPVTNL SVS VENLCTVIW 50  
 ||.|| |..|:..||| :..|..|:||| .|||..|:||| :|||  
 1 MARPALLGELLVLL..WTATVGQVAAATEVQPPVTNL SVS VENLCTIIW 48

51 TWNPPEGASSNC SLWYF SHFGDKQDKKIAPETRRSIEVPLNERICLQVGS 100  
 ||.||| ||.||.||:||| |||:||.||| ||| |||:||| :|||  
 49 TWS PPEGASPN CTLRYF SHFDDQDKKIAPETHRKEELPLDEKICLQVGS 98

101 QCSTNESEKPSILVEKCISPP EGDPESAVTELQ CWHNLSYMKCSWL PGR 150  
 ||| .||| ||| ||.||| ||| ||| ||| ||| ||| ||| ||| |||  
 99 QCSANESEKPSPLVKKCISPP EGDPESAVTELKC CWHNLSYMKCSWL PGR 148

151 NTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFQCSFDLTKVKDSSF EQH 200  
 ||| ||| :||| ||.||| :||| ||| :||| .||| :||| :|||  
 149 NTSPDTHTYTLYYWYSSLEKSRQCENIYREGQHIA CFSFKLTKV. EPSFEHQ 197

201 SVQIMVKDNAGKIKPSENIVPLTSRVKDPPIKKNLSFHNDL YVQWENP 250  
 ||| .||| ||| :||| .||| ||| ||| :||| .||| .||| .|||  
 198 NVQIMVKDNAGKIRPSCKIVSILTSYVKDPPIKHL LKNGALLVQWKNP 247

251 QNFISRCLFVEVEVNNSQTEHNVFYVQEAKCENPEFERNVENTSCFMVP 300  
 ||| .||| ||| ||| :||| :||| .||| .||| :||| .||| :|||  
 248 QNFRSRCLTYEVEVNNTQ TDRHNILEVEEDKCQNS ESDRNMEGTSCFQLP 297

301 GVL PDTLNTVRIRVKTNKL CYEDDKLWSNWSQEMSIGKRNSTLYITMLL 350  
 ||| :||.||| :||| :||| :||| :||| :||| .||| :||| :|||  
 298 GVLADAVYT V RVRVKT NKL CFDDNKL WSDWSEAQSIGKEQN STFYTTMLL 347

351. IVPVIVAGAIIVLLLKLRLKIIIFPPI PDPGKIFKEMFGDQNDTLHWK 400  
 .||| :||.||| :||| :||| :||| :||| :||| :||| :|||  
 348 TIPVFVAVAVI ILLFYLKRLKIIIFPPI PDPGKIFKEMFGDQNDTLHWK 397

401 KYDIYEKQTKEETDSVVL IENLKKASQ 427  
 ||| .||| :||| :||| :|||  
 398 KYDIYEKQSKEETDSVVL IENLKKAA P 424

FIG. 7b